

cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc 368
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala 70
55 60 65

atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc 416
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro 85
75 80

cag gac ctg tac cac gcc cgt tgc ctg tgc cgg cac tgc gtc agc cta 464
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu 100
90 95

cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac 512
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr 115
105 110

cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag gcc 560
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly 130
120 125

acc cac aag gcc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta 608
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu 150
135 140 145

gct tgt gtg tgt gtg cgg ccc cgt gtg atg ggc tag 644
Ala Cys Val Cys Val Arg Pro Arg Val Met Gly 160
155 160

<210> 2
<211> 161
<212> PRT
<213> Homo sapiens

<400> 2
Met Tyr Gln Val Val Ala Phe Leu Ala Met Val Met Gly Thr His Thr
1 5 10 15
Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser
20 25 30
Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro
35 40 45
Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
50 55 60
Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
65 70 75 80
Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
85 90 95
Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
100 105 110
Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro
115 120 125
Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg
130 135 140

Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
145 150 155 160

Gly

<210> 3
<211> 1013
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(507)

<400> 3
atg tac cag gct gtt gca ttc ttg gca atg atc gtg gga acc cac acc 48
Met Tyr Gln Ala Val Ala Phe Leu Ala Met Ile Val Gly Thr His Thr
1 5 10 15
gtc agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc 96
Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys
20 25 30
ccc agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct 144
Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
35 40 45
gca tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa 192
Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
50 55 60
tcc tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct 240
Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
65 70 75 80
cct tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac 288
Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
85 90 95
ctg tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca 336
Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
100 105 110
ggc tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac 384
Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
115 120 125
cag acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat 432
Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His
130 135 140
cgc cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt 480
Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys
145 150 155 160
gtg tgt gtg cgg ccc cgg gtc atg gct tagtcatgct caccacctgc 527
Val Cys Val Arg Pro Arg Val Met Ala
165
ctgaggctga tgcccggttg ggagagaggg ccagggtgac aatcaccttg ccaatgcggg 587
ccgggttcaa gccctccaaa gccctacctg aagcagcagg ctcccgggac aagatggagg 647

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acttggggag aaactctgac ttttgcactt tttggaagca cttttgggaa ggagcagggt 707
ccgcttggtc tgctagagga tgctgtgtg gcattttctac tcaggaacgg actccaaagg 767
cctgctgacc ctggaagcca tactctctggc tcctttcccc tgaatcccc aactctctggc 827
acaggcactt tctccacctc tccccctttg ctttttgttg tgtttgttg tgcatgccaa 887
ctctgcgtgc agccagggtg aattgccttg aaggatggtt ctgaggtgaa agctgtttac 947
gaaagtgaag agatttatcc aaataaacat ctgtgtttaa aaaaaaaaaa aaaaaaaaaa 1007
aaaaaa 1013

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<210> 4
 <211> 169
 <212> PRT
 <213> Mus musculus

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<400> 4
Met Tyr Gln Ala Val Ala Phe Leu Ala Met Ile Val Gly Thr His Thr
  1             5             10
Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys
          20             25
Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
          35             40             45
Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
          50             55             60
Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
          65             70             75             80
Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
          85             90             95
Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
          100            105            110
Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
          115            120            125
Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His
          130            135            140
Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys
          145            150            155            160
Val Cys Val Arg Pro Arg Val Met Ala
          165

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<210> 5
 <211> 155
 <212> PRT
 <213> Homo sapiens

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<400> 5
Met Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Ser
  1             5             10             15

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Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
20 25 30

Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
35 40 45

Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
50 55 60

Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
65 70 75 80

Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
85 90 95

Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
100 105 110

Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
115 120 125

Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
130 135 140

Thr Cys Val Thr Pro Ile Val His His Val Ala
145 150 155

<210> 6

<211> 117

<212> PRT

<213> Homo sapiens

<400> 6

Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu
1 5 10 15

Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys
20 25 30

Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
35 40 45

Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
50 55 60

Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
65 70 75 80

Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
85 90 95

Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Val Ala Gly
100 105 110

Cys Thr Cys Ile Phe
115

<210> 7

<211> 117

<212> PRT

1003551122101

<400> 7

Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala
130 135 140

Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu Arg Arg
 145 150 155 160

Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe
 165 170 175

Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val
 180 185 190

Leu Pro Arg Ser Val
 195

<210> 9
 <211> 1496
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (511)..(987)

<400> 9
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 gaagaaaaag gccaccgagc aaaaaggaac agagaagggg aggagcagtg ctgtgggctc 120
 gcctagggtc gagggccatt atcacctaca aatcagaatg tgggagtgtc attctagagg 180
 tctccattctt tgccattgct gggtogctca gaaaagtgtg atgggggtgt cccattgccca 240
 agaacacgctt ctgcttacca gcagggtgtg acctctttcc ccagaggcac agggaagggaa 300
 ttccagcccc ggttggtgtc cagaggcttc ctctggcggt ggggtacagag gcagagaaaag 360
 aaacccccaaa tgtctcctat gaaaaacaat gtccccgtca tccaggccag atcattctgc 420
 agtgtcaaca gttgagacaa gaagctgggg tcattttctg tgccaaagag tgccctgttct 480
 gcactggcca aggctgttgc attcttggca atg atc gtg gga acc cac acc gtc 534
 Met Ile Val Gly Thr His Thr Val
 1 5

agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc ccc 582
 Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys Pro
 10 15 20

agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct gca 630
 Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser Ala
 25 30 35 40

tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa tcc 678
 Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu Ser
 45 50 55

tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct cct 726
 Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser Pro
 60 65 70

tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac ctg 774
 Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp Leu
 75 80 85

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tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca ggc 822
Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr Gly
90 95 100

tcc cac atg gac cgg ctg ggc aac tcc gtc cca ctt tac cac aac cag 870
Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn Gln
105 110 115 120

acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat cgc 918
Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His Arg
125 130 135

cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt gtg 966
Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys Val
140 145 150

tgt gtg cgg ccc cgg gtc atg gcttagtcat gctcaccacc tgcctgaggc 1017
Cys Val Arg Pro Arg Val Met
155

tgatgcccggtt tggggagaga gggccaggtg tacaatcacc ttgccaatgc gggccggggtt 1077
caagccctcc aaagccctac ctgaagcagc aggcctcccg gacaagatgg aggacttggg 1137
gagaaactct gacttttgca ctttttggaa gcacttttgg gaaggagcag gtcccgcttg 1197
tgctgctaga ggatgctggt gtggcatttc tactcaggaa cggactccaa aggcctgctg 1257
accctggaag ccatactcct ggctccttcc cctgaatcc cccaactcct ggcacaggca 1317
ctttctccac ctctccccc ttgccttttg ttgtgtttgt ttgtgcatgc caactctgcg 1377
tgcagccagg tgtaattgcc ttgaaggatg gttctgaggt gaaagctggt atcgaaagtg 1437
aagagattta tccaaataaa catctgtggt taaaaaaaa aaaaaaaaa aaaaaaaaa 1496

<210> 10
<211> 159
<212> PRT
<213> Mus musculus

<400> 10
Met Ile Val Gly Thr His Thr Val Ser Leu Arg Ile Gln Glu Gly Cys
1 5 10 15

Ser His Leu Pro Ser Cys Cys Pro Ser Lys Glu Gln Glu Pro Pro Glu
20 25 30

Glu Trp Leu Lys Trp Ser Ser Ala Ser Val Ser Pro Pro Glu Pro Leu
35 40 45

Ser His Thr His His Ala Glu Ser Cys Arg Ala Ser Lys Asp Gly Pro
50 55 60

Leu Asn Ser Arg Ala Ile Ser Pro Trp Ser Tyr Glu Leu Asp Arg Asp
65 70 75 80

Leu Asn Arg Val Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro
85 90 95

1003522100


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<210> 11
<211> 27
<212> PRT
<213> Artificial Sequence
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>400> 11
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
  1          5          10          15
Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
          20          25
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<210> 12
<211> 233
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: peptide of Fc
      fragment
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<400> 12																	
Glu	Pro	Lys	Ser	Ala	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala		
1				5					10						15		
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
			20					25					30				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
			35				40					45					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val		
	50					55					60						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
					70					75					80		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
			85						90					95			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
			100					105					110				

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 13

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide of HIV
TAT protein

<400> 13

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 14

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide of HIV
TAT protein

<400> 14

Phe Ile Thr Cys Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln
1 5 10 15

Arg Arg Arg

<210> 15

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

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<400> 15
tagggccagt gaagatgg 18

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 16
tacagcctgc gctccaggca gtagcc 26

<210> 17
<211> 1841
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1555)

<400> 17
ataaaagcgc agcgtgcggg tggcctggat cccgcgcagt ggcccggcg atg tcg ctc 58
Met Ser Leu
1

gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys
85 90 95

gtg agg tgc aat tac aca gag gcc ttc cag act cag acc aga ccc tct 394
Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser
100 105 110 115

ggg ggt aaa tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac 442
Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
120 125 130

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aca gtc tat ttc att ggg gcc cat aat att cct aat gca aat atg aat	490
Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn	
135 140 145	
gaa gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta	538
Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu	
150 155 160	
gac cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg	586
Asp His Ile Met Lys Tyr Lys Lys Cys Val Lys Ala Gly Ser Leu	
165 170 175	
tgg gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa	634
Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu	
180 185 190 195	
gtg aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc	682
Val Asn Phe Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile	
200 205 210	
caa cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag	730
Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln	
215 220 225	
aag aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt	778
Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser	
230 235 240	
gaa ggt gct acg gtg cag ctg act cca tat ttt cct act tgt ggc agc	826
Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser	
245 250 255	
gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc cca caa aca ggc	874
Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly	
260 265 270 275	
gtc cct ttc cct ctg gat aac aac aaa agc aag ccg gga ggc tgg ctg	922
Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu	
280 285 290	
cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg gtg ctg gtg gca	970
Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala	
295 300 305	
ggg atc tat cta atg tgg agg cac gaa agg atc aag aag act tcc ttt	1018
Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe	
310 315 320	
tct acc acc aca cta ctg ccc ccc att aag gtt ctt gtg gtt tac cca	1066
Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro	
325 330 335	
tct gaa ata tgt ttc cat cac aca att tgt tac ttc act gaa ttt ctt	1114
Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu	
340 345 350 355	
caa aac cat tgc aga agt gag gtc atc ctc gaa aag tgg cag aaa aag	1162
Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys	
360 365 370	

aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc act caa aag aag 1210
 Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys
 375 380 385

 gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac gtc aac agt gtg 1258
 Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val
 390 395 400

 tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc agt gag aac tct 1306
 Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
 405 410 415

 caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc agt gat cta aga 1354
 Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
 420 425 430 435

 agc cag att cat ctg cac aaa tac gtg gtg gtc tac ttt aga gag att 1402
 Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
 440 445 450

 gat aca aaa gac gat tac aat gct ctc agt gtc tgc ccc aag tac cac 1450
 Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
 455 460 465

 ctc atg aag gat gcc act gct ttc tgt gca gaa ctt ctc cat gtc aag 1498
 Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys
 470 475 480

 cag cag gtg tca gca gga aaa aga tca caa gcc tgc cac gat ggc tgc 1546
 Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys
 485 490 495

 tgc tcc ttg tagcccccc atgagaagca agagacctta aaggcttctc 1595
 Cys Ser Leu
 500

 atccccacca ttacagggaa aaaacgtgtg atgacacctga agcttactat gcagcctaca 1655
 aacagcctta gtaattaaaa cattttatcac caataaaaatt ttraaatatt gctaactaat 1715
 gtagcattaaa ctaacgattg gaaactacat ttacaacttc aaagctgttt tatacataga 1775
 aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca ataaagcatc 1835
 ttcagc 1841

 <210> 18
 <211> 502
 <212> PRT
 <213> Homo sapiens

 <400> 18
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 1 5 10 15
 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 20 25 30
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
195 200 205

Ala Leu Ile Gln His Ser Thr Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
245 250 255

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
260 265 270

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
275 280 285

Gly Trp Leu Pro Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
290 295 300

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
305 310 315 320

Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
325 330 335

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
340 345 350

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
355 360 365

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
 370 375 380

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
 385 390 395 400

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
 405 410 415

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
 420 425 430

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
 435 440 445

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
 450 455 460

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
 465 470 475 480

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
 485 490 495

Asp Gly Cys Cys Ser Leu
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<210> 19
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 <213> Homo sapiens

<220>
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 Met Ser Leu
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gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
 Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
 5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
 Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
 20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
 Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
 40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
 Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
 55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
 Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
 70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346

Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser	Tyr	Ser	Cys	
85						90					95					
gtg	agg	ctg	cag	tgc	agt	ggt	gcg	atc	atg	gct	cgc	tgc	gac	ctc	aat	394
Val	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Ala	Arg	Cys	Asp	Leu	Asn	
100					105					110					115	
ctt	ctg	ggc	tca	agc	gat	cgt	tct	gct	tca	gcc	tcc	cga	gcg	gct	ggg	442
Leu	Leu	Gly	Ser	Ser	Asp	Arg	Ser	Ala	Ser	Ala	Ser	Arg	Ala	Ala	Gly	
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act	gca	ggc	gtg	ggc	cac	cag	acc	tgg	cta	att	ttt	gta	gtt	ttt	gta	490
Thr	Ala	Gly	Val	Gly	His	Gln	Thr	Trp	Leu	Ile	Phe	Val	Val	Phe	Val	
				135				140						145		
gag	ggg	ggt	ttc	acc	gtg	ttg	ctg	gtc	ttg	aat	tcc	agt	gct	cag	gcg	538
Glu	Gly	Gly	Phe	Thr	Val	Leu	Leu	Val	Leu	Asn	Ser	Ser	Ala	Gln	Ala	
			150				155					160				
atc	tgc	ctg	cct	cgg	ctt	ccc	aaa	gtg	ctg	gga	tta	cag	tgg	aca	ttt	586
Ile	Cys	Leu	Pro	Arg	Leu	Pro	Lys	Val	Leu	Gly	Leu	Gln	Trp	Thr	Phe	
						170						175				
tcc	tac	atc	ggc	ttc	cct	gta	gag	ctg	aac	aca	gtc	tat	ttc	att	ggg	634
Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr	Phe	Ile	Gly	
180						185					190				195	
gcc	cat	aat	att	cct	aat	gca	aat	atg	aat	gaa	gat	ggc	cct	tcc	atg	682
Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	
				200					205					210		
tct	gtg	aat	ttc	acc	tca	cca	ggc	tgc	cta	gac	cac	ata	atg	aaa	tat	730
Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	
				215				220								
aaa	aaa	aag	tgt	gtc	aag	gcc	gga	agc	ctg	tgg	gat	ccg	aac	atc	act	778
Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	
			230				235					240				
gct	tgt	aag	aag	aat	gag	gag	aca	gta	gaa	gtg	aac	ttc	aca	acc	act	826
Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	
				245			250				255					
ccc	ctg	gga	aac	aga	tac	atg	gct	ctt	atc	caa	cac	agc	act	atc	atc	874
Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile	
260						265				270				275		
ggg	ttt	tct	cag	gtg	ttt	gag	cca	cac	cag	aag	aaa	caa	acg	cga	gct	922
Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	
				280					285					290		
tca	gtg	gtg	att	cca	gtg	act	ggg	gat	agt	gaa	ggt	gct	acg	gtg	cag	970
Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	
				295				300					305			
ctg	act	cca	tat	ttt	cct	act	tgt	ggc	agc	gac	tgc	atc	cga	cat	aaa	1018
Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	
				310				315				320				
gga	aca	gtt	gtg	ctc	tgc	cca	caa	aca	ggc	gtc	cct	ttc	cct	ctg	gat	1066
Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	
				325				330				335				

aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser 340 345 350 355	1114
ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp 360 365 370	1162
agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Leu Leu 375 380 385	1210
ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His 390 395 400	1258
cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser 405 410 415	1306
gag gtc atc ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly 420 425 430 435	1354
cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val 440 445 450	1402
ttc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly 455 460 465	1450
aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu 470 475 480	1498
gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His 485 490 495	1546
aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr 500 505 510 515	1594
aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr 520 525 530	1642
gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly 535 540 545	1690
aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccaccc Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu 550 555 560	1739
atgagaagca agagacctta aaggcttctt atcccaccaa ttacaggga aaaacgtgtg	1799
atgatcctga agcttaetat gcagcctaca aacagcctta gtaattaaaa cattttat	1859
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<211> 560
<212> PRT
<213> Homo sapiens

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Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
  20          25          30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
  35          40          45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
  50          55          60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
  65          70          75          80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
  85          90          95

Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
  100         105         110

Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
  115         120         125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
  130         135         140

Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
  145         150         155         160

Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
  165         170         175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
  180         185         190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
  195         200         205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
  210         215         220

Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
  225         230         235         240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
  245         250         255

Thr Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
  260         265         270

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Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
 275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
 290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
 305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
 325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu
 340 345 350

Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr
 355 360 365

Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr
 370 375 380

Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile
 385 390 395 400

Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His
 405 410 415

Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala
 420 425 430

Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp
 435 440 445

Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly
 450 455 460

Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu
 465 470 475 480

Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile
 485 490 495

His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys
 500 505 510

Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys
 515 520 525

Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val
 530 535 540

Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
 545 550 555 560

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 <211> 521
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 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
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Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser
100 105 110

Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
115 120 125

Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn
130 135 140

Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu
145 150 155 160

Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu
165 170 175

Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu
180 185 190

Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile
195 200 205

Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln
210 215 220

Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser
225 230 235 240

Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
245 250 255

Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
260 265 270

Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
275 280 285

Pro Ala Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
290 295 300

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
305 310 315 320

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
325 330 335

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
340 345 350

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 355 360 365
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 370 375 380
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 385 390 395 400
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 405 410 415
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 420 425 430
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 435 440 445
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 450 455 460
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 465 470 475 480
 Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 485 490 495
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 500 505 510
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 515 520
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 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
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 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
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 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95
 Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
 100 105 110
 Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Arg
 115 120 125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140

Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160

Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220

Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255

Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala
340 345 350

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
355 360 365

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
370 375 380

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
385 390 395 400

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
405 410 415

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
420 425 430

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
435 440 445

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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gtacagtggc tgaccactca gaag

24

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 24

ggtggactac aagggtgaac agc

23